40					45					50		
Gly	Arg	Val 55	. Lys	Tyr	Gly	Leu	His 60	A sn	Leu	Gln	Ile	Ser 65
His	Leu	Ser	Ile	Ala 70	Ser	Ser	Gln	. Val	Glu 75	Leu	Val	Asp
Ala	Lys 80	Thr	Ile	Asp	Val	Ala 85	Ile	Gln	Asn	Val	Ser	Val
Val	Phe	Lys	Gly 95	Thr	Leu	Asn	Tyr	Ser 100		Thr	Ser	Ala
Trp 105	Gly	Leu	Gly	Ile	Asn 110	Gln	Ser	Val	Asp	Phe 115		Ile
Asp	Ser	Ala 120	Ile	Asp	Leu	Gln	Ile 125	Asn	Thr	Glu	Leu	Thr 130
Cys	Asp	Ala	Gly	Ser 135	Val	Arg	Thr	Asn	Ala 140	Pro	Asp	Cys
Tyr	Leu 145	Ala	Phe	His	Lys	Leu 150	Leu	Leu	His	Leu	Gln 155	Gly
Glu	Arg	Glu	Pro 160	Gly	Trp	Leu	Lys	Gln 165	Leu	Phe	Thr	Asn
Phe 170	Ile	Ser	Phe	Thr	Leu 175	Lys	Leu	Ile	Leu	Lys 180	Arg	Gln
Val	Cys	Asn 185	Glu	Ile	Asn	Thr	Ile 190	Ser	Asn	Ile	Met	Ala 195
Asp	Phe	Val	Gln	Thr 200	Arg	Ala	Ala	Ser	Ile 205	Leu	Ser	Asp
Gly	Asp 210	Ile	Gly	Val	Asp	Ile 215	Ser	Val	Thr	Gly	Ala 220	Pro
Val	Ile	Thr	Ala 225	Thr	Tyr	Leu	Glu	Ser 230	His	His	Lys	Gly
His 235	Phe	Thr	His	Lys	Asn 240	Val	Ser	Glu	Ala	Phe 245	Pro	Leu
Arg	Ala	Phe 250	Pro	Pro	Gly	Leu	Leu 255	Gly	Asp	Ser	Arg	Met 260
Leu	Tyr	Phe	Trp	Phe 265	Ser	Asp	Gln	Val	Leu 270	Asn	Ser	Leu
Ala	Arg 275	Ala	Ala	Phe	Gln	Glu 280	Gly	Arg	Leu	Val	Leu 285	Ser
Leu	Thr	Gly	Asp	Glu	Phe	Lys	Lys	Val	Leu	Glu	Thr	Gln

290

295

Gly Phe Asp Thr Asn Gln Glu Ile Phe Gln Glu Leu Ser Arg Gly Leu Pro Thr Gly Gln Ala Gln Val Ala Val His 315 Cys Leu Lys Val Pro Lys Ile Ser Cys Gln Asn Arg Gly Val Val Val Ser Ser Ser Val Ala Val Thr Phe Arg Phe 340 Pro Arg Pro Asp Gly Arg Glu Ala Val Ala Tyr Arg Phe Glu Glu Asp Ile Ile Thr Thr Val Gln Ala Ser Tyr Ser 365 370 Gln Lys Lys Leu Phe Leu His Leu Leu Asp Phe Gln Cys Val Pro Ala Ser Gly Arg Ala Gly Ser Ser Ala Asn Leu 395 Ser Val Ala Leu Arg Thr Glu Ala Lys Ala Val Ser Asn 405 Leu Thr Glu Ser Arg Ser Glu Ser Leu Gln Ser Ser Leu Arg Ser Leu Ile Ala Thr Val Gly Ile Pro Glu Val Met 430 435 Ser Arg Leu Glu Val Ala Phe Thr Ala Leu Met Asn Ser 445 450 Lys Gly Leu Asp Leu Phe Glu Ile Ile Asn Pro Glu Ile 460 Ile Thr Leu Asp Gly Cys Leu Leu Leu Gln Met Asp Phe 475 Gly Phe Pro Lys His Leu Leu Val Asp Phe Leu Gln Ser 485 490

Leu Ser 495

- (2) INFORMATION FOR SEQ ID NO: 3:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1428 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) (iv) (ix) (x)	MOLECULE TYPE: cDNA HYPOTHETICAL: ANTI-SENSE: FEATURE: (A) NAME: Structural coding s mature human CETP (B) LOCATION: PUBLICATION INFORMATION: (A) AUTHORS: Drayna, Dennis, et (B) TITLE: Cloning and sequence human cholesteryl e transfer cDNA (C) JOURNAL: Nature (D) VOLUME: 327 (E) ISSUE: (F) PAGES: 632 - 634 (G) DATE: 18-JUN-1987 (K) RELEVANT RESIDUES IN SEQ ID N	al. eing of ester
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:3	:
TGCTCCAAAG	GCACCTCGCA CGAGGCAGGC ATCGTGTGCC GC	CATCACCAA 50
GCCTGCCCTC	CTGGTGTTGA ACCACGAGAC TGCCAAGGTG AT	rccagaccg 100
CCTTCCAGCG	AGCCAGCTAC CCAGATATCA CGGGCGAGAA GC	GCCATGATG 150
CTCCTTGGCC	AAGTCAAGTA TGGGTTGCAC AACATCCAGA TO	CAGCCACTT 200
GTCCATCGCC	AGCAGCCAGG TGGAGCTGGT GGAAGCCAAG TG	CCATTGATG 250
TCTCCATTCA	GAACGTGTCT GTGGTCTTCA AGGGGACCCT GA	AAGTATGGC 300
TACACCACTG	CCTGGTGGCT GGGTATTGAT CAGTCCATTG AC	CTTCGAGAT 350
CGACTCTGCC	ATTGACCTCC AGATCAACAC ACAGCTGACC TO	GTGACTCTG 400
GTAGAGTGCG	GACCGATGCC CCTGACTGCT ACCTGTCTTT CC	CATAAGCTG 450
CTCCTGCATC	TCCAAGGGGA GCGAGAGCCT GGGTGGATCA AC	GCAGCTGTT 500
CACAAATTTC	ATCTCCTTCA CCCTGAAGCT GGTCCTGAAG GC	GACAGATCT 550
GCAAAGAGAT	CAACGTCATC TCTAACATCA TGGCCGATTT TC	GTCCAGACA 600
AGGGCTGCCA	GCATCCTTTC AGATGGAGAC ATTGGGGTGG AC	CATTTCCCT 650
GACAGGTGAT	CCCGTCATCA CAGCCTCCTA CCTGGAGTCC CA	ATCACAAGG 700
GTCATTTCAT	CTACAAGAAT GTCTCAGAGG ACCTCCCCCT CC	CCCACCTTC 750
TCGCCCACAC	TGCTGGGGGA CTCCCGCATG CTGTACTTCT GG	GTTCTCTGA 800
GCGAGTCTTC	CACTCGCTGG CCAAGGTAGC TTTCCAGGAT GG	GCCGCCTCA 850
TGCTCAGCCT	GATGGGAGAC GAGTTCAAGG CAGTGCTGGA GA	ACCTGGGGC 900

TTCAACACCA	ACCAGGAAAT	CTTCCAAGAG	GTTGTCGGCG	GCTTCCCCAG	950
CCAGGCCCAA	GTCACCGTCC	ACTGCCTCAA	GATGCCCAAG	ATCTCCTGCC	1000
AAAACAAGGG	AGTCGTGGTC	AATTCTTCAG	TGATGGTGAA	ATTCCTCTTT	1050
CCACGCCCAG	ACCAGCAACA	TTCTGTAGCT	TACACATTTG	AAGAGGATAT	1100
CGTGACTACC	GTCCAGGCCT	CCTATTCTAA	GAAAAAGCTC	TTCTTAAGCC	1150
TCTTGGATTT	CCAGATTACA	CCAAAGACTG	TTTCCAACTT	GACTGAGAGC	1200
AGCTCCGAGT	CCATCCAGAG	CTTCCTGCAG	TCAATGATCA	CCGCTGTGGG	1250
CATCCCTGAG	GTCATGTCTC	GGCTCGAGGT	AGTGTTTACA	GCCCTCATGA	1300
ACAGCAAAGG	CGTGAGCCTC	TTCGACATCA	TCAACCCTGA	GATTATCACT	1350
CGAGATGGCT	TCCTGCTGCT	GCAGATGGAC	TTTGGCTTCC	CTGAGCACCT	1400
GCTGGTGGAT	TTCCTCCAGA	GCTTGAGC			1428

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS: (i)

(A) LENGTH: 476 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

HYPOTHETICAL: (iii)

(iv) ANTI-SENSE:

(ix) FEATURE:

> (A) NAME: Amino acid sequence of mature human CETP

(B) LOCATION:

(x) PUBLICATION INFORMATION:

> (A) AUTHORS: Drayna, Dennis, et al.

(B) TITLE: Cloning and sequencing of human cholesteryl ester transfer cDNA

(C) JOURNAL: Nature

(D) VOLUME: 327

(E) ISSUE: (F) PAGES:

632 - 634

(G) DATE: 18-JUN-1987

(K) RELEVANT RESIDUES IN SEQ ID NO:4: FROM 1 TO 476

SEQUENCE DESCRIPTION: SEQ ID NO: 4: (xi)

Cys Ser Lys Gly Thr Ser His Glu Ala Gly Ile Val Cys

Arg Ile Thr Lys Pro Ala Leu Leu Val Leu Asn His Glu

Thr Ala Lys Val Ile Gln Thr Ala Phe Gln Arg Ala Ser

Tyr 40	Pro	Asp	Ile	Thr	Gly 45	Glu	Lys	Ala	Met	Met 50	Leu	Leu
Gly	Gln	Val 55	Lys	Tyr	Gly	Leu	His 60	Asn	Ile	Gln	Ile	Ser 65
His	Leu	Ser	Ile	Ala 70	Ser	Ser	Gln	Val	Glu 75	Leu	Val	Glu
Ala	Lys 80	Ser	Ile	Asp	Val	Ser 85	Ile	Gln	Asn	Val	Ser 90	Val
Val	Phe	Lys	Gly 95	Thr	Leu	Lys	Tyr	Gly 100	Tyr	Thr	Thr	Ala
Trp 105	Trp	Leu	Gly	Ile	Asp 110	Gln	Ser	Ile	Asp	Phe 115	Glu	Ile
Asp	Ser	Ala 120	Ile	Asp	Leu	Gln	Ile 125	Asn	Thr	Gln	Leu	Thr 130
Cys	Asp	Ser	Gly	Arg 135	Val	Arg	Thr	Asp	Ala 140	Pro	Asp	Cys
Tyr	Leu 145	Ser	Phe	His	Lys	Leu 150	Leu	Leu	His	Leu	Gln 155	Gly
Glu	Arg	Glu	Pro 160	Gly	Trp	Ile	Lys	Gln 165	Leu	Phe	Thr	Asn
Phe 170	Ile	Ser	Phe	Thr	Leu 175	Lys	Leu	Val	Leu	Lys 180	Gly	Gln
Ile	Cys	Lys 185	Glu	Ile	Asn	Val	Ile 190	Ser	Asn	Ile	Met	Ala 195
Asp	Phe	Val	Gln	Thr 200	Arg	Ala	Ala	Ser	Ile 205	Leu	Ser	Asp
Gly	Asp 210	Ile	Gly	Val	Asp	Ile 215	Ser	Leu	Thr	Gly	Asp 220	Pro
Val	Ile	Thr	Ala 225	Ser	Tyr	Leu	Glu	Ser 230	His	His	Lys	Gly
His 235	Phe	Ile	Tyr	Lys	Asn 240	Val	Ser	Glu	Asp	Leu 245	Pro	Leu
Pro	Thr	Phe 250	Ser	Pro	Thr	Leu	Leu 255	Gly	Asp	Ser	Arg	Met 260
Leu	Tyr	Phe	Trp	Phe 265	Ser	Glu	Arg	Val	Phe 270	His	Ser	Leu
Ala	Lys 275	Val	Ala	Phe	Gln	Asp 280	Gly	Arg	Leu	Met	Leu 285	Ser

Leu	Met	Gly	Asp 290	Glu	Phe	Lys	Ala	Val 295	Leu	Glu	Thr	Trp
Gly 300	Phe	Asn	Thr	Asn	Gln 305	Glu	Ile	Phe	Gln	Glu 310	Val	Val
Gly	Gly	Phe 315	Pro	Ser	Gln	Ala	Gln 320	Val	Thr	Val	His	Cys 325
Leu	Lys	Met	Pro	Lys 330	Ile	Ser	Cys	Gln	Asn 335	Lys	Gly	Val
Val	Val 340	Asn	Ser	Ser	Val	Met 345	Val	Lys	Phe	Leu	Phe 350	Pro
Arg	Pro	Asp	Gln 355	Gln	His	Ser	Val	Ala 360	Tyr	Thr	Phe	Glu
Glu 365	Asp	Ile	Val	Thr	Thr 370	Val	Gln	Ala	Ser	Tyr 375	Ser	Lys
Lys	Lys	Leu 380	Phe	Leu	Ser	Leu	Leu 385	Asp	Phe	Gln	Ile	Thr 390
Pro	Lys	Thr	Val	Ser 395	Asn	Leu	Thr	Glu	Ser 400	Ser	Ser	Glu
Ser	Ile 405	Gln	Ser	Phe	Leu	Gln 410	Ser	Met	Ile	Thr	Ala 415	Val
Gly	Ile	Pro	Glu 420	Val	Met	Ser	Arg	Leu 425	Glu	Val	Val	Phe
Thr 430	Ala	Leu	Met	Asn	Ser 435	Lys	Gly	Val	Ser	Leu 440	Phe	Asp
Ile	Ile	Asn 445	Pro	Glu	Ile	Ile	Thr 450	Arg	Asp	Gly	Phe	Leu 455
Leu	Leu	Gln	Met	Asp 460	Phe	Gly	Phe	Pro	Glu 465	His	Leu	Leu

(2) INFORMATION FOR SEQ ID NO: 5:

Val Asp Phe Leu Gln Ser Leu Ser

470

- SEQUENCE CHARACTERISTICS: (i)

- (A) LENGTH: 169 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE:
- HYPOTHETICAL: (iii)
- (iv) ANTI-SENSE:
- (ix) FEATURE:

	(A) NAME: (B) LOCATION:	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:5:	
GCGGCCGCCA	TGCAGTACAT CAAGGCCAAC TCCAAGTTCA TCGGCATCAC	50
GGAGCGCTTC	CCCCGCCCAG ATGGCCGAGA AGCTGTGGCC TACAGGTTTG	100
AGGAGGATAT	CTTCGGTTTT CCCAAGCACC TGCTGGTGGA TTTCCTGCAG	150
AGCCTGAGCT	AGCGGCCGC	169
(i) (ii) (iii) (iv)	AATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: (A) LENGTH: 169 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear MOLECULE TYPE: DNA HYPOTHETICAL: ANTI-SENSE: FEATURE: (A) NAME: Complementary strand to SEQ ID (B) LOCATION: 1 to 169	NO:5
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:6:	
GCGGCCGCTA	GCTCAGGCTC TGCAGGAAAT CCACCAGCAG GTGCTTGGGA	50
AAACCGAAGA	TATCCTCCTC AAACCTGTAG GCCACAGCTT CTCGGCCATC	100
TGGGCGGGGG	AAGCGCTCCG TGATGCCGAT GAACTTGGAG TTGGCCTTGA	150
TGTACTGCAT	CGCGGCCGC	169
(2) INFORM (i) (ii) (iii) (iv) (ix)	MATION FOR SEQ ID NO:7: SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear MOLECULE TYPE: peptide HYPOTHETICAL: ANTI-SENSE: FEATURE: amino acid sequence of peptide enco by bases 10 to 159 of SEQ ID NO:5 (A) NAME: (B) LOCATION:	oded
(xi) S	EQUENCE DESCRIPTION: SEQ ID NO:7:	
Met Gln Tyr 1	: Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile 5 10	
Thr Glu Arg 15	Phe Pro Arg Pro Asp Gly Arg Glu Ala Val 20 25	

Ala Tyr Arg Phe 30	Glu Glu	Asp Ile	Phe Gly	Phe	Pro	Lys
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His Leu Leu Val Asp Phe Leu Gln Ser Leu Ser 40 45 50

(2)	INFORMA	TION FOR SEQ ID NO:8: SEQUENCE CHARACTERISTICS: (A) LENGTH: 1608 base pairs
		(B) TYPE: nucleic acid (C) STRANDEDNESS: Single
	(33)	(D) TOPOLOGY: linear MOLECULE TYPE:
	(iii)	HYPOTHETICAL:
		ANTI-SENSE: FEATURE:
	, ,	(A) NAME: translational stop codon (B) LOCATION: 1606 - 1608

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGCGCTGATG	ATGTTGTTGA	TTCTTCTAAA	TCTTTTGTGA	TGGAAAACTT	50
TTCTTCGTAC	CACGGGACTA	AACCTGGTTA	TGTAGATTCC	ATTCAAAAAG	100
GTATACAAAA	GCCAAAATCT	GGTACACAAG	GAAATTATGA	CGATGATTGG	150
AAAGGGTTTT	ATAGTACCGA	CAATAAATAC	GACGCTGCGG	GATACTCTGT	200
AGATAATGAA	AACCCGCTCT	CTGGAAAAGC	TGGAGGCGTG	GTCAAAGTGA	250
CGTATCCAGG	ACTGACGAAG	GTTCTCGCAC	TAAAAGTGGA	TAATGCCGAA	300
ACTATTAAGA	AAGAGTTAGG	TTTAAGTCTC	ACTGAACCGT	TGATGGAGCA	350
AGTCGGAACG	GAAGAGTTTA	TCAAAAGGTT	CGGTGATGGT	GCTTCGCGTG	400
TAGTGCTCAG	CCTTCCCTTC	GCTGAGGGGA	GTTCTAGCGT	TGAATATATT	450
AATAACTGGG	AACAGGCGAA	AGCGTTAAGC	GTAGAACTTG	AGATTAATTT	500
TGAAACCCGT	GGAAAACGTG	GCCAAGATGC	GATGTATGAG	TATATGGCTC	550
AAGCCTGTGC	AGGAAATCGT	GTCAGGCGAT	CAGTAGGTAG	CTCATTGTCA	600

TGCATAAATC	TTGATTGGGA	TGTCATAAGG	GATAAAACTA	AGACAAAGAT	650
AGAGTCTTTG	AAAGAGCATG	GCCCTATCAA	AAATAAAATG	AGCGAAAGTC	700
CCAATAAAAC	AGTATCTGAG	GAAAAAGCTA	AACAATACCT	AGAAGAATTT	750
CATCAAACGG	CATTAGAGCA	TCCTGAATTG	TCAGAACTTA	AAACCGTTAC	800
TGGGACCAAT	CCTGTATTCG	CTGGGGCTAA	CTATGCGGCG	TGGGCAGTAA	850
ACGTTGCGCA	AGTTATCGAT	AGCGAAACAG	CTGATAATTT	GGAAAAGACA	900
ACTGCTGCTC	TTTCGATACT	TCCTGGTATC	GGTAGCGTAA	TGGGCATTGC	950
AGACGGTGCC	GTTCACCACA	ATACAGAAGA	GATAGTGGCA	CAATCAATAG	1000
CTTTATCGTC	TTTAATGGTT	GCTCAAGCTA	TTCCATTGGT	AGGAGAGCTA	1050
GTTGATATTG	GTTTCGCTGC	ATATAATTT	GTAGAGAGTA	TTATCAATTT	1100
ATTTCAAGTA	GTTCATAATT	CGTATAATCG	TCCCGCGTAT	TCTCCGGGGC	1150
ATAAAACGCA	ACCATTTCTT	CATGACGGGT	ATGCTGTCAG	TTGGAACACT	1200
GTTGAAGATT	CGATAATCCG	AACTGGTTTT	CAAGGGGAGA	GTGGGCACGA	1250
CATAAAAATT	ACTGCTGAAA	ATACCCCGCT	TCCAATCGCG	GGTGTCCTAC	1300
TACCGACTAT	TCCTGGAAAG	CTGGACGTTA	ATAAGTCCAA	GACTCATATT	1350
TCCGTAAATG	GTCGGAAAAT	AAGGATGCGT	TGCAGAGCTA	TAGACGGTGA	1400
TGTAACTTTT	TGTCGCCCTA	AATCTCCTGT	TTATGTTGGT	AATGGTGTGC	1450
ATGCGAATCT	TCACGTGGCA	TTTCACAGAA	GCAGCTCGGA	GAAAATTCAT	1500
TCTAATGAAA	TTTCGTCGGA	TTCCATAGGC	GTTCTTGGGT	ACCAGAAAAC	1550

AGTAGATCAC ACCAAGGTTA ATTCTAAGCT ATCGCTATTT TTTGAAATCA 1600

AAAGCTGA 1608

(2) INFORMATION FOR SEO ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 535 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL:
- (iv) ANTI-SENSE:
- (ix) FEATURE:
 - (A) NAME:
 - (B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Gly Ala Asp Asp Val Val Asp Ser Ser Lys Ser Phe Val Met
1 10

Glu Asn Phe Ser Ser Tyr His Gly Thr Lys Pro Gly Tyr Val 15 20 25

Asp Ser Ile Gln Lys Gly Ile Gln Lys Pro Lys Ser Gly Thr 30 35 40

Gln Gly Asn Tyr Asp Asp Trp Lys Gly Phe Tyr Ser Thr 45 50 55

Asp Asn Lys Tyr Asp Ala Ala Gly Tyr Ser Val Asp Asn Glu 65 70

Asn Pro Leu Ser Gly Lys Ala Gly Gly Val Val Lys Val Thr 75 80

Tyr Pro Gly Leu Thr Lys Val Leu Ala Leu Lys Val Asp Asn 85 90 95

Ala Glu Thr Ile Lys Lys Glu Leu Gly Leu Ser Leu Thr Glu
100 105 110

Pro Leu Met Glu Gln Val Gly Thr Glu Glu Phe Ile Lys Arg 115 120 125

Phe Gly Asp Gly Ala Ser Arg Val Val Leu Ser Leu Pro Phe 130 135 140

Ala Glu Gly Ser Ser Ser Val Glu Tyr Ile Asn Asn Trp Glu 145 150

Gln Ala Lys Ala Leu Ser Val Glu Leu Glu Ile Asn Phe Glu 155 160 165

Thr Arq Gly Lys Arg Gly Gln Asp Ala Met Tyr Glu Tyr Met

HER HARRING MAIN

	170					175					180		
Ala	Gln	Ala 185	Cys	Ala	Gly	Asn	Arg 190	Val	Arg	Arg	Ser	Val 195	Gly
Ser	Ser	Leu	Ser 200	Cys	Ile	Asn	Leu	Asp 205		Asp	Val	Ile	Arg 210
Asp	Lys	Thr	Lys	Thr 215	Lys	Ile	Glu	Ser	Leu 220	Lys	Glu	His	Gly
Pro 225	Ile	Lys	Asn	Lys	Met 230	Ser	Glu	Ser	Pro	Asn 235	Lys	Thr	Va]
Ser	Glu 240	Glu	Lys	Ala	Lys	Gln 245	Tyr	Leu	Glu	Glu	Phe 250	His	Glr
Thr	Ala	Leu 255	Glu	His	Pro	Glu	Leu 260	Ser	Glu	Leu	Lys	Thr 265	Va]
Thr	Gly	Thr	Asn 270	Pro	Val	Phe	Ala	Gly 275	Ala	Asn	Tyr	Ala	Ala 280
Trp	Ala	Val	Asn	Val 285	Ala	Gln	Val	Ile	Asp 290	Ser	Glu	Thr	Ala
Asp 295	Asn	Leu	Glu	Lys	Thr 300	Thr	Ala	Ala	Leu	Ser 305	Ile	Leu	Pro
Gly	Ile 310	Gly	Ser	Val	Met	Gly 315	Ile	Ala	Asp	Gly	Ala 320	Val	His
His	Asn	Thr 325	Glu	Glu	Ile	Val	Ala 330	Gln	Ser	Ile	Ala	Leu 335	Ser
Ser	Leu	Met	Val 340	Ala	Gln	Ala	Ile	Pro 345	Leu	Val	Gly	Glu	Leu 350
Val	Asp	Ile	Gly	Phe 355	Ala	Ala	Tyr	Asn	Phe 360	Val	Glu	Ser	Ile
Ile 365	Asn	Leu	Phe	Gln	Val 370	Val	His	Asn	Ser	Tyr 375	Asn	Arg	Pro
Ala	Tyr 380	Ser	Pro	Gly	His	Lys 385	Thr	Gln	Pro	Phe	Leu 390	His	Asp
Gly	Tyr	Ala 395	Val	Ser	Trp	Asn	Thr 400	Val	Glu	Asp	Ser	Ile 405	Ile
Arg	Thr	Gly	Phe 410	Gln	Gly	Glu	Ser	Gly 415	His	Asp	Ile	Lys	Ile 420
Thr	Ala	Glu	Asn	Thr 425	Pro	Leu	Pro	Ile	Ala 430	Gly	Val	Leu	Leu
Pro 435	Thr	Ile	Pro	Gly	Lys 440	Leu	Asp	Val	Asn	Lys 445	Ser	Lys	Thr

His Ile Ser Val Asn Gly Arg Lys Ile Arg Met Arg Cys Arg 455

Ala Ile Asp Gly Asp Val Thr Phe Cys Arg Pro Lys Ser Pro 465

Val Tyr Val Gly Asn Gly Val His Ala Asn Leu His Val Ala

Phe His Arg Ser Ser Ser Glu Lys Ile His Ser Asn Glu Ile 495

Ser Ser Asp Ser Ile Gly Val Leu Gly Tyr Gln Lys Thr Val 510

Asp His Thr Lys Val Asn Ser Lys Leu Ser Leu Phe Phe Glu 520 525

Ile Lys Ser 535

- (2) INFORMATION FOR SEQ ID NO:10
 - SEQUENCE CHARACTERISTICS: (i)
 - (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 MOLECULE TYPE: protein
 - (ii)
 - (iii) HYPOTHETICAL:
 - (iv) ANTI-SENSE:
 - (ix) FEATURE:
 - (A) NAME:
 - (B) LOCATION:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro

Lys Val Ser Ala Ser His Leu Glu 15

(1) GENERAL INFORMATION:

Thomas, Lawrence J. (i)APPLICANT:

(ii) TITLE OF INVENTION: PLASMID-BASED VACCINE FOR

TREATING ATHEROSCLEROSIS

(iii) NUMBER OF SEQUENCES: 10

(iv) CORRESPONDENCE ADDRESS:

ADDRESSEE: Yankwich & Associates STREET: 130 Bishop Allen Drive CITY: Cambridge (A)

(B)

(C) CITY:

Massachusetts (D) STATE:

(E) COUNTRY: USA

(F) ZIP: 02139

COMPUTER READABLE FORM: (∇)

MEDIUM TYPE: Floppy disk (A)

COMPUTER: IBM PC compatible (B)

OPERATING SYSTEM: Windows 95/98 (C)

SOFTWARE: Word 97 (D)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: (not yet assigned)

(B) FILING DATE: 30 April 2001

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION: 08/640,713

(B) FILING DATE: 01 May 1996 (01.05.96)

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION: 08/802,967

FILING DATE: 21 February 1997 (21.02.97) (B)

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION: 09/171,969

(B) FILING DATE: 29 October 1998 (29.10.98)

ATTORNEY/AGENT INFORMATION: (viii)

(A) NAME: Leon R. Yankwich

(B) REGISTRATION NUMBER: 30,237

(C) REFERENCE/DOCKET NUMBER: TCS-414.2 US-1

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1488 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(ix) FEATURE: Structural coding sequence for

mature rabbit CETP

- (A) NAME:
- (B) LOCATION:
- (x) PUBLICATION INFORMATION:
- (A) AUTHORS: Nagashima, Mariko, et al.
- (B) TITLE: Cloning and mRNA tissue distribution of rabbit

cholesteryl ester transfer

protein

- (C) JOURNAL: J. Lipid Res.
- (D) VOLUME: 29
- (E) ISSUE:
- (F) PAGES: 1643 1649
- (G) DATE: 1988
- (K) RELEVANT RESIDUES IN SEQ ID NO:1: FROM 1 TO 1488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TGTCCCAAAG G	CGCCTCCTA	CGAGGCTGGC	ATCGTGTGTC	GCATCACCAA	50
GCCCGCCCTC T	TGGTGTTGA	ACCAAGAGAC	GGCCAAGGTG	GTCCAGACGG	100
CCTTCCAGCG C	CGCCGGCTAT	CCGGACGTCA	GCGGCGAGAG	GGCCGTGATG	150
CTCCTCGGCC G	GGTCAAGTA	CGGGCTGCAC	AACCTCCAGA	TCAGCCACCT	200
GTCCATCGCC A	AGCAGCCAGG	TGGAGCTGGT	GGACGCCAAG	ACCATCGACG	250
TCGCCATCCA C	BAACGTGTCC	GTGGTCTTCA	AGGGGACCCT	GAACTACAGC	300
TACACGAGTG (CCTGGGGGTT	GGGCATCAAT	CAGTCTGTCG	ACTTCGAGAT	350
CGACTCTGCC A	ATTGACCTCC	AGATCAACAC	AGAGCTGACC	TGCGACGCTG	400
GCAGTGTGCG (CACCAATGCC	CCCGACTGCT	ACCTGGCTTT	CCATAAACTG	450
CTCCTGCACC 1	TCCAGGGGGA	GCGCGAGCCG	GGGTGGCTCA	AGCAGCTCTT	500
CACAAACTTC A	ATCTCCTTCA	CCCTGAAGCT	GATTCTGAAG	CGACAGGTCT	550
GCAATGAGAT (CAACACCATC	TCCAACATCA	TGGCTGACTT	TGTCCAGACG	600
AGGGCCGCCA (GCATCCTCTC	AGATGGAGAC	ATCGGGGTGG	ACATTTCCGT	650
GACGGGGGCC (CCTGTCATCA	CAGCCACCTA	CCTGGAGTCC	CATCACAAGG	700
GTCACTTCAC (GCACAAGAAC	GTCTCCGAGG	CCTTCCCCCT	CCGCGCCTTC	750
CCGCCCGGTC '	TTCTGGGGGA	CTCCCGCATG	CTCTACTTCT	GGTTCTCCGA	800
TCAAGTGCTC .	AACTCCCTGG	CCAGGGCCGC	CTTCCAGGAG	GGCCGTCTCG	850
TGCTCAGCCT	GACAGGGGAT	GAGTTCAAGA	AAGTGCTGGA	GACCCAGGGT	900
TTCGACACCA	ACCAGGAAAT	CTTCCAGGAG	CTTTCCAGAG	GCCTTCCCAC	950
CGGCCAGGCC	CAGGTAGCCG	TCCACTGCCT	TAAGGTGCCC	AAGATCTCCT	1000

GCCAGAACCG	GGGTGTCGTG	GTGTCTTCTT	CCGTCGCCGT	GACGTTCCGC		1050
TTCCCCCGCC	CAGATGGCCG	AGAAGCTGTG	GCCTACAGGT	TTGAGGAGGA		1100
TATCATCACC	ACCGTCCAGG	CCTCCTACTC	CCAGAAAAAG	CTCTTCCTAC		1150
ACCTCTTGGA	TTTCCAGTGC	GTGCCGGCCA	GCGGAAGGGC	AGGCAGCTCA		1200
GCAAATCTCT	CCGTGGCCCT	CAGGACTGAG	GCTAAGGCTG	TTTCCAACCT		1250
GACTGAGAGC	CGCTCCGAGT	CCCTGCAGAG	CTCTCTCCGC	TCCCTGATCG		1300
CCACGGTGGG	CATCCCGGAG	GTCATGTCTC	GGCTCGAGGT	GGCGTTCACA		1350
GCCCTCATGA	ACAGCAAAGG	CCTGGACCTC	TTCGAAATCA	TCAACCCCGA		1400
GATTATCACT	CTCGATGGCT	GCCTGCTGCT	GCAGATGGAC	TTCGGTTTTC		1450
CCAAGCACCT	GCTGGTGGAT	TTCCTGCAGA	GCCTGAGC		1488	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:

496 amino acids

(B) TYPE:

amino acid

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL:
- (iv) ANTI-SENSE:
- (ix) FEATURE:
- $\mbox{(A)}\mbox{ NAME:}$ Amino acid sequence for mature rabbit CETP protein.
 - (B) LOCATION:
- (x) PUBLICATION INFORMATION:
- (A) AUTHORS: Nagashima, Mariko, et al.
- (B) TITLE: Cloning and mRNA tissue

distribution of rabbit

cholesteryl ester transfer

protein

- (C) JOURNAL: J. Lipid Res.
- (D) VOLUME: 29
- (E) ISSUE:
- (F) PAGES: 1643 1649
- (G) DATE: 1988
- (K) RELEVANT RESIDUES IN SEQ ID NO:2: FROM 1 TO 496
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Cys Pro Lys Gly Ala Ser Tyr Glu Ala Gly Ile Val Cys
1 5 10

Arg Ile Thr Lys Pro Ala Leu Leu Val Leu Asn Gln Glu
15 20 25

njji

- Thr Ala Lys Val Val Gln Thr Ala Phe Gln Arg Ala Gly 30 35
- Tyr Pro Asp Val Ser Gly Glu Arg Ala Val Met Leu Leu 40 45 50
- Gly Arg Val Lys Tyr Gly Leu His Asn Leu Gln Ile Ser 55 60 65
- His Leu Ser Ile Ala Ser Ser Gln Val Glu Leu Val Asp
 70 75
- Ala Lys Thr Ile Asp Val Ala Ile Gln Asn Val Ser Val 80 85 90
- Val Phe Lys Gly Thr Leu Asn Tyr Ser Tyr Thr Ser Ala 95 100
- Trp Gly Leu Gly Ile Asn Gln Ser Val Asp Phe Glu Ile 105 110 115
- Asp Ser Ala Ile Asp Leu Gln Ile Asn Thr Glu Leu Thr 120 125 130
- Cys Asp Ala Gly Ser Val Arg Thr Asn Ala Pro Asp Cys 135 140
- Tyr Leu Ala Phe His Lys Leu Leu Leu His Leu Gln Gly 145 150 155
- Glu Arg Glu Pro Gly Trp Leu Lys Gln Leu Phe Thr Asn 160 165
- Phe Ile Ser Phe Thr Leu Lys Leu Ile Leu Lys Arg Gln 170 175 180
- Val Cys Asn Glu Ile Asn Thr Ile Ser Asn Ile Met Ala 185 190 195
- Asp Phe Val Gln Thr Arg Ala Ala Ser Ile Leu Ser Asp 200 205
- Gly Asp Ile Gly Val Asp Ile Ser Val Thr Gly Ala Pro 210 215 220
- Val Ile Thr Ala Thr Tyr Leu Glu Ser His His Lys Gly
 225 230
- His Phe Thr His Lys Asn Val Ser Glu Ala Phe Pro Leu 235 240 245
- Arg Ala Phe Pro Pro Gly Leu Leu Gly Asp Ser Arg Met 250 255 260
- Leu Tyr Phe Trp Phe Ser Asp Gln Val Leu Asn Ser Leu

265 270

Ala Arg Ala Ala Phe Gln Glu Gly Arg Leu Val Leu Ser 275 280 285

Leu Thr Gly Asp Glu Phe Lys Lys Val Leu Glu Thr Gln 290 295

Gly Phe Asp Thr Asn Gln Glu Ile Phe Gln Glu Leu Ser 300 305 310

Arg Gly Leu Pro Thr Gly Gln Ala Gln Val Ala Val His 315 320 325

Cys Leu Lys Val Pro Lys Ile Ser Cys Gln Asn Arg Gly 330 335

Val Val Val Ser Ser Ser Val Ala Val Thr Phe Arg Phe 340 345 350

Pro Arg Pro Asp Gly Arg Glu Ala Val Ala Tyr Arg Phe 355 360

Glu Glu Asp Ile Ile Thr Thr Val Gln Ala Ser Tyr Ser 365 370 375

Gln Lys Lys Leu Phe Leu His Leu Leu Asp Phe Gln Cys 380 385 390

Val Pro Ala Ser Gly Arg Ala Gly Ser Ser Ala Asn Leu 395 400

Ser Val Ala Leu Arg Thr Glu Ala Lys Ala Val Ser Asn 405 410 415

Leu Thr Glu Ser Arg Ser Glu Ser Leu Gln Ser Ser Leu 420 425

Arg Ser Leu Ile Ala Thr Val Gly Ile Pro Glu Val Met 430 440

Ser Arg Leu Glu Val Ala Phe Thr Ala Leu Met Asn Ser 445 450 455

Lys Gly Leu Asp Leu Phe Glu Ile Ile Asn Pro Glu Ile 460 465

Ile Thr Leu Asp Gly Cys Leu Leu Leu Gln Met Asp Phe 470 475 480

Gly Phe Pro Lys His Leu Leu Val Asp Phe Leu Gln Ser 485 490

Leu Ser 495

/2\ TNEOD	MATION FOD	SEQ ID NO: 3:								
(i)		ARACTERISTICS:								
(1)		TH: 1428 base p	pairs							
	(B) TYPE	nucleic aci	ld							
(C) STRAN	DEDNESS: si									
(-)		LOGY: linear								
(ii)										
(iii)	HYPOTHETIC	AL:								
(iv)	ANTI-SENSE	:								
(ix)	FEATURE:									
(A) NAME: Structural coding sequence for										
mature huma	n CETP									
	(B) LOCA									
	CATION INFO									
(A) AUTHO	RS: Dray	na, Dennis, et al.	_							
		ing and sequencing	of							
	steryl este	r								
transfer cD	NA									
	IAL: Natu	re								
(D) VOLUM										
(E) ISSUE		62.4								
	632									
(G) DATE:	18-JUN-198	S IN SEQ ID NO:3:	FPOM 1 TO 1428							
(K) RELEV	ANI KESIDUE	S IN SEQ ID NO.3.	TROM 1 10 1420							
(xi)	SEOUENCE I	ESCRIPTION: SEQ ID	NO:3:							
(/		~								
TGCTCCAAAG	GCACCTCGCA	CGAGGCAGGC ATCGTGT	GCC GCATCACCAA	50						
GCCTGCCCTC	CTGGTGTTGA	ACCACGAGAC TGCCAAG	GTG ATCCAGACCG	100						
		GG2 G2 F2 FG2 GGGGGG3	an a addanman ma	150						
CCTTCCAGCG	AGCCAGCTAC	CCAGATATCA CGGGCGA	GAA GGCCATGATG	150						
CTT CCTTTTC CCC	3 3 CTC 3 3 CT3	TGGGTTGCAC AACATCC	NGN TONGOCACTT	200						
CTCCTTGGCC	AAGTCAAGTA	IGGGIIGCAC AACAICC	AGA ICAGCCACII	200						
amaaa maaaa	7 CC7 CCC7 CC	TGGAGCTGGT GGAAGCC	AAC TCCATTGATG	250						
GICCAICGCC	AGCAGCCAGG	IGGACTGGT GGAACC	AAO ICCAIIGAIG	250						
ጥሮጥሮ ሮልጥ ሞሮል	GAACGTGTCT	GTGGTCTTCA AGGGGAC	CCT GAAGTATGGC	300						
ICICCATICA	OAACOIGICI	01001011011 11000010	001 01110 2111 0 0							
TACACCACTG	CCTGGTGGCT	GGGTATTGAT CAGTCCA	TTG ACTTCGAGAT	350						
11.011001101										
CGACTCTGCC	ATTGACCTCC	AGATCAACAC ACAGCTG	ACC TGTGACTCTG	400						
GTAGAGTGCG	GACCGATGCC	CCTGACTGCT ACCTGTC	TTT CCATAAGCTG	450						
CTCCTGCATC	TCCAAGGGGA	GCGAGAGCCT GGGTGGA	TCA AGCAGCTGTT	500						
CACAAATTTC	ATCTCCTTCA	CCCTGAAGCT GGTCCTG	BAAG GGACAGATCT	550						
				600						
GCAAAGAGAT	CAACGTCATC	TCTAACATCA TGGCCGA	ATTT TGTCCAGACA	600						
a documents	a a y maammea	707F007070 70F00000	TGG ACATTTCCCT	650						
AGGGCTGCCA	GCATCCTTTC	AGAIGGAGAC AIIGGGG	TIGG ACATIICCCI	050						
CV הא המתהמא היי	ርርርርጥር አ <i>ጥር</i> አ	CAGCCTCCTA CCTGGAG	TTCC CATCACAAGG	700						
CACACCIDAL	CCCGICAICA	CAUCUICCIA CCIGGAC	JICC CITCHICITION	, 50						
ርተCΣተተሞሪΣ ተ	СТАСААСААТ	GTCTCAGAGG ACCTCCC	CCT CCCCACCTTC	750						
C. C										

TCGCCCACAC TGCTGGGGGA CTCCCGCATG CTGTACTTCT GGTTCTCTGA 800 GCGAGTCTTC CACTCGCTGG CCAAGGTAGC TTTCCAGGAT GGCCGCCTCA 850 TGCTCAGCCT GATGGGAGAC GAGTTCAAGG CAGTGCTGGA GACCTGGGGC 900 TTCAACACCA ACCAGGAAAT CTTCCAAGAG GTTGTCGGCG GCTTCCCCAG 950 CCAGGCCCAA GTCACCGTCC ACTGCCTCAA GATGCCCAAG ATCTCCTGCC 1000 AAAACAAGGG AGTCGTGGTC AATTCTTCAG TGATGGTGAA ATTCCTCTTT 1050 CCACGCCCAG ACCAGCAACA TTCTGTAGCT TACACATTTG AAGAGGATAT 1100 CGTGACTACC GTCCAGGCCT CCTATTCTAA GAAAAAGCTC TTCTTAAGCC 1150 TCTTGGATTT CCAGATTACA CCAAAGACTG TTTCCAACTT GACTGAGAGC 1200 AGCTCCGAGT CCATCCAGAG CTTCCTGCAG TCAATGATCA CCGCTGTGGG 1250 CATCCCTGAG GTCATGTCTC GGCTCGAGGT AGTGTTTACA GCCCTCATGA 1300 ACAGCAAAGG CGTGAGCCTC TTCGACATCA TCAACCCTGA GATTATCACT 1350 CGAGATGGCT TCCTGCTGCT GCAGATGGAC TTTGGCTTCC CTGAGCACCT 1400 1428 GCTGGTGGAT TTCCTCCAGA GCTTGAGC

```
(2) INFORMATION FOR SEQ ID NO: 4:
```

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 476 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL:
- (iv) ANTI-SENSE:
- (ix) FEATURE:

(A) NAME: Amino acid sequence of mature human

CETP

- (B) LOCATION:
- (x) PUBLICATION INFORMATION:
- (A) AUTHORS: Drayna, Dennis, et al.
- (B) TITLE: Cloning and sequencing of human

cholesteryl ester transfer cDNA

- (C) JOURNAL: Nature
 (D) VOLUME: 327
- (E) ISSUE:
- (F) PAGES: 632 634
- (G) DATE: 18-JUN-1987
- (K) RELEVANT RESIDUES IN SEQ ID NO:4: FROM 1 TO 476
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

DECEMBER OF

- Cys Ser Lys Gly Thr Ser His Glu Ala Gly Ile Val Cys $1 \hspace{1cm} 5 \hspace{1cm} 10$
- Arg Ile Thr Lys Pro Ala Leu Leu Val Leu Asn His Glu 15 20 25
- Thr Ala Lys Val Ile Gln Thr Ala Phe Gln Arg Ala Ser 30 35
- Tyr Pro Asp Ile Thr Gly Glu Lys Ala Met Met Leu Leu 40 45 50
- Gly Gln Val Lys Tyr Gly Leu His Asn Ile Gln Ile Ser 55 60 65
- His Leu Ser Ile Ala Ser Ser Gln Val Glu Leu Val Glu
 70 75
- Ala Lys Ser Ile Asp Val Ser Ile Gln Asn Val Ser Val 80 85 90
- Val Phe Lys Gly Thr Leu Lys Tyr Gly Tyr Thr Thr Ala 95 100
- Trp Trp Leu Gly Ile Asp Gln Ser Ile Asp Phe Glu Ile 105 110 115
- Asp Ser Ala Ile Asp Leu Gln Ile Asn Thr Gln Leu Thr 120 125 130
- Cys Asp Ser Gly Arg Val Arg Thr Asp Ala Pro Asp Cys 135 140
- Tyr Leu Ser Phe His Lys Leu Leu Leu His Leu Gln Gly 145 150 155
- Glu Arg Glu Pro Gly Trp Ile Lys Gln Leu Phe Thr Asn 160 165
- Phe Ile Ser Phe Thr Leu Lys Leu Val Leu Lys Gly Gln 170 175 180
- Ile Cys Lys Glu Ile Asn Val Ile Ser Asn Ile Met Ala 185 190 195
- Asp Phe Val Gln Thr Arg Ala Ala Ser Ile Leu Ser Asp 200 205
- Gly Asp Ile Gly Val Asp Ile Ser Leu Thr Gly Asp Pro 210 215 220
- Val Ile Thr Ala Ser Tyr Leu Glu Ser His His Lys Gly
- His Phe Ile Tyr Lys Asn Val Ser Glu Asp Leu Pro Leu 235 240 245

Pro Thr Phe Ser Pro Thr Leu Leu Gly Asp Ser Arg Met 255 250 Leu Tyr Phe Trp Phe Ser Glu Arg Val Phe His Ser Leu Ala Lys Val Ala Phe Gln Asp Gly Arg Leu Met Leu Ser 275 Leu Met Gly Asp Glu Phe Lys Ala Val Leu Glu Thr Trp Gly Phe Asn Thr Asn Gln Glu Ile Phe Gln Glu Val Val 305 Gly Gly Phe Pro Ser Gln Ala Gln Val Thr Val His Cys 315 320 Leu Lys Met Pro Lys Ile Ser Cys Gln Asn Lys Gly Val 330 Val Val Asn Ser Ser Val Met Val Lys Phe Leu Phe Pro 345 . 340 Arq Pro Asp Gln Gln His Ser Val Ala Tyr Thr Phe Glu Glu Asp Ile Val Thr Thr Val Gln Ala Ser Tyr Ser Lys 370 Lys Lys Leu Phe Leu Ser Leu Leu Asp Phe Gln Ile Thr 380 385 Pro Lys Thr Val Ser Asn Leu Thr Glu Ser Ser Ser Glu 395 Ser Ile Gln Ser Phe Leu Gln Ser Met Ile Thr Ala Val 410 405

Gly Ile Pro Glu Val Met Ser Arg Leu Glu Val Val Phe

Thr Ala Leu Met Asn Ser Lys Gly Val Ser Leu Phe Asp 430 435 440

Ile Ile Asn Pro Glu Ile Ile Thr Arg Asp Gly Phe Leu 445 450 455

Leu Leu Gln Met Asp Phe Gly Phe Pro Glu His Leu Leu
460 465

Val Asp Phe Leu Gln Ser Leu Ser 470 475

(2) INFORMATION FOR SEQ ID NO: 5:

(A)		ME: CAT	ION:											
*	(2	ci) s	SEQUE	ENCE	DESC	CRIPI	CION:	SEÇ	Q ID	NO: 7	7 :			
Met 1	Gln	Tyr	Ile	Lys 5	Ala	Asn	Ser	Lys	Phe 10	Ile	Gly	Ile		
Thr	Glu 15	Arg	Phe	Pro	Arg	Pro 20	Asp	Gly	Arg	Glu	Ala 25	Val		
Ala	Tyr	Arg	Phe 30	Glu	Glu	Asp	Ile	Phe 35	Gly	Phe	Pro	Lys		
His 40	Leu	Leu	Val	Asp	Phe 45	Leu	Gln	Ser	Leu	Ser 50				
(i) (A) (B) (C) (ii) (ii) (iv) (ix) (A)	(2) INFORMATION FOR SEQ ID NO:8: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1608 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: Single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: (iii) HYPOTHETICAL: (iv) ANTI-SENSE: (ix) FEATURE: (A) NAME: translational stop codon (B) LOCATION: 1606 - 1608													
GGC	GCTG	ATG	ATGT	TGTT	GA T	TCTT	CTAA	A TC	TTTT	GTGA	TGG	AAAAC	${f T}{f T}$	50
TTC	TTCG	TAC	CACG	GGAC	TA A	ACCT	GGTT	A TG	TAGA	TTCC	ATT	CAAAA	AG	100
GTA	TACA	AAA	GCCA	TAAA	CT G	GTAC	ACAA	G GA	TTAA	'ATGA	CGA	TGATT	GG	150
AAA	GGGI	TTT	ATAG	TACC	GA C	'AA'TA	ATAA	C GA	CGCI	'GCGG	GAT	ACTCT	GT	200
AGA	TAAT	GAA	AACC	CGCT	CT C	TGGA	AAAG	C TO	GAGG	CGTG	GTC	'AAAGT	'GA	250
CGT	TATCO	CAGG	ACTG	ACGA	AG G	TTCT	'CGCA	C TA	AAAG	TGGA	TAA	TGCCG	AA	300
ACT	TTATTA	AAGA	AAGA	GTTA	.GG T	TTAA	GTCT	'C AC	CTGAA	CCGT	TGA	TGGAG	CA	350
AGT	CGGF	AACG	GAAG	AGTT	TA T	CAAA	AGGT	T CO	GTGA	TGGT	GCI	TCGCG	TG	400
TAC	TGCT	rcag	CCTT	CCCT	TC C	SCTGA	rdggg	A GT	TCTA	AGCGI	TGA	ATATA	TT	450
AAT	raac'i	rggg	AACA	\GGCG	AA A	AGCGT	TAAC	C G	ragaz	ACTTO	G AGA	TAATTA	TT	500
		agam.	aan 7	3 7 CC	ıma a	יו מסטי	. C 3 TTC	ומ מז	\ mcimi	\ TT/CT 7\ C	יים אי	רא ידיכיכי	יידירי	550

AAGCCTGTGC AGGAAATCGT GTCAGGCGAT CAGTAGGTAG CTCATTGTCA

TGCATAAATC TTGATTGGGA TGTCATAAGG GATAAAACTA AGACAAAGAT 650 700 AGAGTCTTTG AAAGAGCATG GCCCTATCAA AAATAAAATG AGCGAAAGTC CCAATAAAAC AGTATCTGAG GAAAAAGCTA AACAATACCT AGAAGAATTT 750 CATCAAACGG CATTAGAGCA TCCTGAATTG TCAGAACTTA AAACCGTTAC 800 TGGGACCAAT CCTGTATTCG CTGGGGCTAA CTATGCGGCG TGGGCAGTAA 850 ACGTTGCGCA AGTTATCGAT AGCGAAACAG CTGATAATTT GGAAAAGACA 900 ACTGCTGCTC TTTCGATACT TCCTGGTATC GGTAGCGTAA TGGGCATTGC 950 AGACGGTGCC GTTCACCACA ATACAGAAGA GATAGTGGCA CAATCAATAG 1000 CTTTATCGTC TTTAATGGTT GCTCAAGCTA TTCCATTGGT AGGAGAGCTA 1050 GTTGATATTG GTTTCGCTGC ATATAATTTT GTAGAGAGTA TTATCAATTT 1100 ATTTCAAGTA GTTCATAATT CGTATAATCG TCCCGCGTAT TCTCCGGGGC 1150 ATAAAACGCA ACCATTTCTT CATGACGGGT ATGCTGTCAG TTGGAACACT 1200 GTTGAAGATT CGATAATCCG AACTGGTTTT CAAGGGGAGA GTGGGCACGA 1250 CATAAAAATT ACTGCTGAAA ATACCCCGCT TCCAATCGCG GGTGTCCTAC 1300 TACCGACTAT TCCTGGAAAG CTGGACGTTA ATAAGTCCAA GACTCATATT 1350 TCCGTAAATG GTCGGAAAAT AAGGATGCGT TGCAGAGCTA TAGACGGTGA 1400 TGTAACTTTT TGTCGCCCTA AATCTCCTGT TTATGTTGGT AATGGTGTGC 1450 ATGCGAATCT TCACGTGGCA TTTCACAGAA GCAGCTCGGA GAAAATTCAT 1500 TCTAATGAAA TTTCGTCGGA TTCCATAGGC GTTCTTGGGT ACCAGAAAAC 1550 AGTAGATCAC ACCAAGGTTA ATTCTAAGCT ATCGCTATTT TTTGAAATCA 1600 1608 AAAGCTGA

- (2) INFORMATION FOR SEQ ID NO:9:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 535 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL:
- (iv) ANTI-SENSE:
- (ix) FEATURE:

- (A) NAME:
- (B) LOCATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

- Gly Ala Asp Asp Val Val Asp Ser Ser Lys Ser Phe Val Met 1 5 10
- Glu Asn Phe Ser Ser Tyr His Gly Thr Lys Pro Gly Tyr Val
- Asp Ser Ile Gln Lys Gly Ile Gln Lys Pro Lys Ser Gly Thr 30 35 40
- Gln Gly Asn Tyr Asp Asp Asp Trp Lys Gly Phe Tyr Ser Thr 45 50 55
- Asp Asn Lys Tyr Asp Ala Ala Gly Tyr Ser Val Asp Asn Glu
 60 65 70
- Asn Pro Leu Ser Gly Lys Ala Gly Gly Val Val Lys Val Thr
- Tyr Pro Gly Leu Thr Lys Val Leu Ala Leu Lys Val Asp Asn 85 90 95
- Ala Glu Thr Ile Lys Lys Glu Leu Gly Leu Ser Leu Thr Glu 100 105 110
- Pro Leu Met Glu Gln Val Gly Thr Glu Glu Phe Ile Lys Arg
- Phe Gly Asp Gly Ala Ser Arg Val Val Leu Ser Leu Pro Phe 130 135 140
- Ala Glu Gly Ser Ser Ser Val Glu Tyr Ile Asn Asn Trp Glu
 145 150
- Gln Ala Lys Ala Leu Ser Val Glu Leu Glu Ile Asn Phe Glu 155 160 165
- Thr Arg Gly Lys Arg Gly Gln Asp Ala Met Tyr Glu Tyr Met
- Ala Gln Ala Cys Ala Gly Asn Arg Val Arg Arg Ser Val Gly
 185 190 195
- Ser Ser Leu Ser Cys Ile Asn Leu Asp Trp Asp Val Ile Arg 200 205 210
- Asp Lys Thr Lys Thr Lys Ile Glu Ser Leu Lys Glu His Gly 215 220
- Pro Ile Lys Asn Lys Met Ser Glu Ser Pro Asn Lys Thr Val 225 230 235
- Ser Glu Glu Lys Ala Lys Gln Tyr Leu Glu Glu Phe His Gln 240 245 250
- Thr Ala Leu Glu His Pro Glu Leu Ser Glu Leu Lys Thr Val 255 260 265

- Thr Gly Thr Asn Pro Val Phe Ala Gly Ala Asn Tyr Ala Ala 270 275 280
- Trp Ala Val Asn Val Ala Gln Val Ile Asp Ser Glu Thr Ala 285 290
- Asp Asn Leu Glu Lys Thr Thr Ala Ala Leu Ser Ile Leu Pro 295 300 305
- Gly Ile Gly Ser Val Met Gly Ile Ala Asp Gly Ala Val His 310 315 320
- His Asn Thr Glu Glu Ile Val Ala Gln Ser Ile Ala Leu Ser 325 330 335
- Ser Leu Met Val Ala Gln Ala Ile Pro Leu Val Gly Glu Leu 340 345 350
- Val Asp Ile Gly Phe Ala Ala Tyr Asn Phe Val Glu Ser Ile 355 360
- Ile Asn Leu Phe Gln Val Val His Asn Ser Tyr Asn Arg Pro 365 370 375
- Ala Tyr Ser Pro Gly His Lys Thr Gln Pro Phe Leu His Asp 380 385 390
- Gly Tyr Ala Val Ser Trp Asn Thr Val Glu Asp Ser Ile Ile 395 400 405
- Arg Thr Gly Phe Gln Gly Glu Ser Gly His Asp Ile Lys Ile 410 415 420
- Thr Ala Glu Asn Thr Pro Leu Pro Ile Ala Gly Val Leu Leu 425 430
- Pro Thr Ile Pro Gly Lys Leu Asp Val Asn Lys Ser Lys Thr 435 440 445
- His Ile Ser Val Asn Gly Arg Lys Ile Arg Met Arg Cys Arg 450 455 460
- Ala Ile Asp Gly Asp Val Thr Phe Cys Arg Pro Lys Ser Pro 465 470 475
- Val Tyr Val Gly Asn Gly Val His Ala Asn Leu His Val Ala 480 485 490
- Phe His Arg Ser Ser Ser Glu Lys Ile His Ser Asn Glu Ile 495 500
- Ser Ser Asp Ser Ile Gly Val Leu Gly Tyr Gln Lys Thr Val 505 510 515
- Asp His Thr Lys Val Asn Ser Lys Leu Ser Leu Phe Phe Glu 520 530

Ile Lys Ser 535

- (2) INFORMATION FOR SEQ ID NO:10
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL:
- (iv) ANTI-SENSE:
- (ix) FEATURE:
- (A) NAME:
- (B) LOCATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro 1 5 10

Lys Val Ser Ala Ser His Leu Glu 15 20

SEQUENCE LISTING

- GENERAL INFORMATION: (1)
 - (i) APPLICANT: Thomas, Lawrence J.
 - (ii) TITLE OF INVENTION: PLASMID-BASED VACCINE FOR TREATING ATHEROSCLEROSIS
 - (iii) NUMBER OF SEQUENCES: 10
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Banner & Witcoff, Ltd.
 - (B) STREET: 75 State Street, Suite 2300 (C) CITY: Boston

 - (C) CITY: Boston
 (D) STATE: Massachusetts
 (E) COUNTRY: USA

 - (F) ZIP: 02109-1807
 - COMPUTER READABLE FORM: (v)
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: WordPerfect 6.1
 - CURRENT APPLICATION DATA: (vi)
 - (A) APPLICATION NUMBER: (not yet assigned)
 - (B) FILING DATE: 01 May 1997 (01.05.97)
 - (C) CLASSIFICATION:
 - PRIOR APPLICATION DATA:
 - (A) APPLICATION: 08/640,713
 - (B) FILING DATE: 01 May 1996 (01.05.96)
 - PRIOR APPLICATION DATA:
 - (A) APPLICATION: 08/802,967
 - (B) FILING DATE: 21 February 1997 (21.02.97)
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Leon R. Yankwich
 - (B) REGISTRATION NUMBER: 30,237
 - (C) REFERENCE/DOCKET NUMBER: TCS 414.1 PCT (05872)
- INFORMATION FOR SEO ID NO: 1: (2)
 - SEQUENCE CHARACTERISTICS: (i)
 - (A) LENGTH: 1488 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - MOLECULE TYPE: CDNA (ii)
 - HYPOTHETICAL: (iii)
 - ANTI-SENSE: (iv)
 - FEATURE: Structural coding sequence for (ix)mature rabbit CETP
 - (A) NAME:
 - (B) LOCATION:
 - (x)PUBLICATION INFORMATION:
 - (A) AUTHORS: Nagashima, Mariko, et al.

PCT/US97/07294 WO 97/41227

31

(B) TITLE: Cloning and mRNA tissue distribution of rabbit cholesteryl ester transfer protein

(C) JOURNAL: J. Lipid Res.

29

1643 - 1649

(D) VOLUME: (E) ISSUE: (F) PAGES: (G) DATE: 1988

(K) RELEVANT RESIDUES IN SEQ ID NO:1: FROM 1 TO

1488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

50	GCATCACCAA	ATCGTGTGTC	CGAGGCTGGC	GCGCCTCCTA	TGTCCCAAAG
100	GTCCAGACGG	GGCCAAGGTG	ACCAAGAGAC	TTGGTGTTGA	GCCCGCCCTC
150	GGCCGTGATG	GCGGCGAGAG	CCGGACGTCA	CGCCGGCTAT	CCTTCCAGCG
200	TCAGCCACCT	AACCTCCAGA	CGGGCTGCAC	GGGTCAAGTA	CTCCTCGGCC
250	ACCATCGACG	GGACGCCAAG	TGGAGCTGGT	AGCAGCCAGG	GTCCATCGCC
300	GAACTACAGC	AGGGGACCCT	GTGGTCTTCA	GAACGTGTCC	TCGCCATCCA
350	ACTTCGAGAT	CAGTCTGTCG	GGGCATCAAT	CCTGGGGGTT	TACACGAGTG
400	TGCGACGCTG	AGAGCTGACC	AGATCAACAC	ATTGACCTCC	CGACTCTGCC
450	CCATAAACTG	ACCTGGCTTT	CCCGACTGCT	CACCAATGCC	GCAGTGTGCG
500	AGCAGCTCTT	GGGTGGCTCA	GCGCGAGCCG	TCCAGGGGGA	CTCCTGCACC
550	CGACAGGTCT	GATTCTGAAG	CCCTGAAGCT	ATCTCCTTCA	CACAAACTTC
600	TGTCCAGACG	TGGCTGACTT	TCCAACATCA	CAACACCATC	GCAATGAGAT
650	ACATTTCCGT	ATCGGGGTGG	AGATGGAGAC	GCATCCTCTC	AGGGCCGCCA
700	CATCACAAGG	CCTGGAGTCC	CAGCCACCTA	CCTGTCATCA	GACGGGGGCC
750	CCGCGCCTTC	CCTTCCCCCT	GTCTCCGAGG	GCACAAGAAC	GTCACTTCAC
800	GGTTCTCCGA	CTCTACTTCT	CTCCCGCATG	TTCTGGGGGA	CCGCCCGGTC
850	GGCCGTCTCG	CTTCCAGGAG	CCAGGGCCGC	AACTCCCTGG	TCAAGTGCTC
900	GACCCAGGGT	AAGTGCTGGA	GAGTTCAAGA	GACAGGGGAT	TGCTCAGCCT
950	GCCTTCCCAC	CTTTCCAGAG	CTTCCAGGAG	ACCAGGAAAT	TTCGACACCA
1000	AAGATCTCCT	TAAGGTGCCC	TCCACTGCCT	CAGGTAGCCG	CGGCCAGGCC
1050	GACGTTCCGC	CCGTCGCCGT	GTGTCTTCTT	GGGTGTCGTG	GCCAGAACCG
1100	TTGAGGAGGA	GCCTACAGGT	AGAAGCTGTG	CAGATGGCCG	TTCCCCCGCC

TATCATCACC	ACCGTCCAGG	CCTCCTACTC	CCAGAAAAAG	CTCTTCCTAC	1150
ACCTCTTGGA	TTTCCAGTGC	GTGCCGGCCA	GCGGAAGGGC	AGGCAGCTCA	1200
GCAAATCTCT	CCGTGGCCCT	CAGGACTGAG	GCTAAGGCTG	TTTCCAACCT	1250
GACTGAGAGC	CGCTCCGAGT	CCCTGCAGAG	CTCTCTCCGC	TCCCTGATCG	1300
CCACGGTGGG	CATCCCGGAG	GTCATGTCTC	GGCTCGAGGT	GGCGTTCACA	1350
GCCCTCATGA	ACAGCAAAGG	CCTGGACCTC	TTCGAAATCA	TCAACCCCGA	1400
GATTATCACT	CTCGATGGCT	GCCTGCTGCT	GCAGATGGAC	TTCGGTTTTC	1450
CCAAGCACCT	GCTGGTGGAT	TTCCTGCAGA	GCCTGAGC		1488

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 496 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL:
- (iv) ANTI-SENSE:
- (ix) FEATURE:
 - (A) NAME: Amino acid sequence for mature rabbit CETP protein.
 - (B) LOCATION:
- (x) PUBLICATION INFORMATION:
 - (A) AUTHORS: Nagashima, Mariko, et al.
 - (B) TITLE: Cloning and mRNA tissue distribution of rabbit cholesteryl ester transfer protein
 - (C) JOURNAL: J. Lipid Res.
 - (D) VOLUME: 29
 - (E) ISSUE:
 - (F) PAGES: 1643 1649
 - (G) DATE: 1988
 - (K) RELEVANT RESIDUES IN SEQ ID NO:2: FROM 1 TO 496
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Cys Pro Lys Gly Ala Ser Tyr Glu Ala Gly Ile Val Cys

5 10

Arg Ile Thr Lys Pro Ala Leu Leu Val Leu Asn Gln Glu
15 20 25

Thr Ala Lys Val Val Gln Thr Ala Phe Gln Arg Ala Gly 30 35

Tyr Pro Asp Val Ser Gly Glu Arg Ala Val Met Leu Leu